

-102-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Israeli, Ron S.
Heston, Warren D.W.
Fair, William R.
- (ii) TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
- (iii) NUMBER OF SEQUENCES: 38
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham
(B) STREET: 30 Rockefeller Plaza
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States of America
(F) ZIP: 10112
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 1747/41426
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 977-9550
(B) TELEFAX: (212) 664-0525
(C) TELEX: 422523 COOP UI

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2653 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
(F) TISSUE TYPE: Carcinoma

103

-103-

(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate-Specific Membrane Antigen

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 262..2511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCAAAGGG GCCGGATTTC CTTCTCCTGG AGGCAGATGT TGCCTCTCTC TCTCGCTCGG	60
ATTGGTTTCAG TGCACTCTAG AAACACTGCT GTGGTGGAGA AACTGGACCC CAGGTCTGGA	120
GCGAATTCCA GCCTGCAGGG CTGATAAGCG AGGCATTAGT GAGATTGAGA GAGACTTTAC	180
CCCGCCGTGG TGGTTGGAGG GCGCGCAGTA GAGCAGCAGC ACAGGCGCGG GTCCCGGGAG	240
GCCGGCTCTG CTCGCGCCGA G ATG TGG AAT CTC CTT CAC GAA ACC GAC TCG	291
Met Trp Asn Leu Leu His Glu Thr Asp Ser	10
1 5	
GCT GTG GCC ACC GCG CGC CGC CCG CGC TGG CTG TGC GCT GGG GCG CTG	339
Ala Val Ala Thr Ala Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu	25
15 20	
GTG CTG GCG GGT GGC TTC TTT CTC CTC GGC TTC CTC TTC GGG TGG TTT	387
Val Leu Ala Gly Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe	40
30 35	
ATA AAA TCC TCC AAT GAA GCT ACT AAC ATT ACT CCA AAG CAT AAT ATG	435
Ile Lys Ser Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met	55
45 50	
AAA GCA TTT TTG GAT GAA TTG AAA GCT GAG AAC ATC AAG AAG TTC TTA	483
Lys Ala Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu	70
60 65	
TAT AAT TTT ACA CAG ATA CCA CAT TTA GCA GGA ACA GAA CAA AAC TTT	531
Tyr Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe	90
75 80	
CAG CTT GCA AAG CAA ATT CAA TCC CAG TGG AAA GAA TTT GGC CTG GAT	579
Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp	105
95 100	
TCT GTT GAG CTA GCA CAT TAT GAT GTC CTG TTG TCC TAC CCA AAT AAG	627
Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys	120
110 115	
ACT CAT CCC AAC TAC ATC TCA ATA ATT AAT GAA GAT GGA AAT GAG ATT	675
Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile	135
125 130	
TTC AAC ACA TCA TTA TTT GAA CCA CCT CCT CCA GGA TAT GAA AAT GTT	723
Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val	150
140 145	
TCG GAT ATT GTA CCA CCT TTC AGT GCT TTC TCT CCT CAA GGA ATG CCA	771
Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser Pro Gln Gly Met Pro	170
155 160 165	

-104-

GAG GGC GAT CTA GTG TAT GTT AAC TAT GCA CGA ACT GAA GAC TTC TTT	819
Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe	
175 180 185	
AAA TTG GAA CGG GAC ATG AAA ATC AAT TGC TCT GGG AAA ATT GTA ATT	867
Lys Leu Glu Arg Asp Met Lys Ile Asn Cys Ser Gly Lys Ile Val Ile	
190 195 200	
GCC AGA TAT GGG AAA GTT TTC AGA GGA AAT AAG GTT AAA AAT GCC CAG	915
Ala Arg Tyr Gly Lys Val Phe Arg Gly Asn Lys Val Lys Asn Ala Gln	
205 210 215	
CTG GCA GGG GCC AAA GGA GTC ATT CTC TAC TCC GAC CCT GCT GAC TAC	963
Leu Ala Gly Ala Lys Gly Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr	
220 225 230	
TTT GCT CCT GGG GTG AAG TCC TAT CCA GAT GGT TGG AAT CTT CCT GGA	1011
Phe Ala Pro Gly Val Lys Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly	
235 240 245 250	
GGT GGT GTC CAG CGT GGA AAT ATC CTA AAT CTG AAT GGT GCA GGA GAC	1059
Gly Gly Val Gln Arg Gly Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp	
255 260 265	
CCT CTC ACA CCA GGT TAC CCA GCA AAT GAA TAT GCT TAT AGG CGT GGA	1107
Pro Leu Thr Pro Gly Tyr Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly	
270 275 280	
ATT GCA GAG GCT GTT GGT CTT CCA AGT ATT CCT GTT CAT CCA ATT GGA	1155
Ile Ala Glu Ala Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly	
285 290 295	
TAC TAT GAT GCA CAG AAG CTC CTA GAA AAA ATG GGT GGC TCA GCA CCA	1203
Tyr Tyr Asp Ala Gln Lys Leu Leu Glu Lys Met Gly Gly Ser Ala Pro	
300 305 310	
CCA GAT AGC AGC TGG AGA GGA AGT CTC AAA GTG CCC TAC AAT GTT GGA	1251
Pro Asp Ser Ser Trp Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly	
315 320 325 330	
CCT GGC TTT ACT GGA AAC TTT TCT ACA CAA AAA GTC AAG ATG CAC ATC	1299
Pro Gly Phe Thr Gly Asn Phe Ser Thr Gln Lys Val Lys Met His Ile	
335 340 345	
CAC TCT ACC AAT GAA GTG ACA AGA ATT TAC AAT GTG ATA GGT ACT CTC	1347
His Ser Thr Asn Glu Val Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu	
350 355 360	
AGA GGA GCA GTG GAA CCA GAC AGA TAT GTC ATT CTG GGA GGT CAC CGG	1395
Arg Gly Ala Val Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg	
365 370 375	
GAC TCA TGG GTG TTT GGT GGT ATT GAC CCT CAG AGT GGA GCA GCT GTT	1443
Asp Ser Trp Val Phe Gly Gly Ile Asp Pro Gln Ser Gly Ala Ala Val	
380 385 390	
GTT CAT GAA ATT GTG AGG AGC TTT GGA ACA CTG AAA AAG GAA GGG TGG	1491
Val His Glu Ile Val Arg Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp	
395 400 405 410	
AGA CCT AGA AGA ACA ATT TTG TTT GCA AGC TGG GAT GCA GAA GAA TTT	1539
Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe	

-105-

415										420										425										
GGT	CTT	CTT	GGT	TCT	ACT	GAG	TGG	GCA	GAG	GAG	AAT	TCA	AGA	CTC	CTT															1587
Gly	Leu	Leu	Gly	Ser	Thr	Glu	Trp	Ala	Glu	Glu	Asn	Ser	Arg	Leu	Leu															
			430					435					440																	
CAA	GAG	CGT	GGC	GTG	GCT	TAT	ATT	AAT	GCT	GAC	TCA	TCT	ATA	GAA	GGA															1635
Gln	Glu	Arg	Gly	Val	Ala	Tyr	Ile	Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly															
			445				450					455																		
AAC	TAC	ACT	CTG	AGA	GTT	GAT	TGT	ACA	CCG	CTG	ATG	TAC	AGC	TTG	GTA															1683
Asn	Tyr	Thr	Leu	Arg	Val	Asp	Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val															
			460			465					470																			
CAC	AAC	CTA	ACA	AAA	GAG	CTG	AAA	AGC	CCT	GAT	GAA	GGC	TTT	GAA	GGC															1731
His	Asn	Leu	Thr	Lys	Glu	Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly															
					480					485				490																
AAA	TCT	CTT	TAT	GAA	AGT	TGG	ACT	AAA	AAA	AGT	CCT	TCC	CCA	GAG	TTC															1779
Lys	Ser	Leu	Tyr	Glu	Ser	Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe															
				495				500					505																	
AGT	GGC	ATG	CCC	AGG	ATA	AGC	AAA	TTG	GGA	TCT	GGA	AAT	GAT	TTT	GAG															1827
Ser	Gly	Met	Pro	Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu															
			510				515					520																		
GTG	TTC	TTC	CAA	CGA	CTT	GGA	ATT	GCT	TCA	GGC	AGA	GCA	CGG	TAT	ACT															1875
Val	Phe	Phe	Gln	Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr															
			525				530					535																		
AAA	AAT	TGG	GAA	ACA	AAC	AAA	TTC	AGC	GGC	TAT	CCA	CTG	TAT	CAC	AGT															1923
Lys	Asn	Trp	Glu	Thr	Asn	Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser															
			540			545					550																			
GTC	TAT	GAA	ACA	TAT	GAG	TTG	GTG	GAA	AAG	TTT	TAT	GAT	CCA	ATG	TTT															1971
Val	Tyr	Glu	Thr	Tyr	Glu	Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe															
					560					565					570															
AAA	TAT	CAC	CTC	ACT	GTG	GCC	CAG	GTT	CGA	GGA	GGG	ATG	GTG	TTT	GAG															2019
Lys	Tyr	His	Leu	Thr	Val	Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe	Glu															
				575			580					585																		
CTA	GCC	AAT	TCC	ATA	GTG	CTC	CCT	TTT	GAT	TGT	CGA	GAT	TAT	GCT	GTA															2067
Leu	Ala	Asn	Ser	Ile	Val	Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr	Ala	Val															
			590				595					600																		
GTT	TTA	AGA	AAG	TAT	GCT	GAC	AAA	ATC	TAC	AGT	ATT	TCT	ATG	AAA	CAT															2115
Val	Leu	Arg	Lys	Tyr	Ala	Asp	Lys	Ile	Tyr	Ser	Ile	Ser	Met	Lys	His															
			605			610					615																			
CCA	CAG	GAA	ATG	AAG	ACA	TAC	AGT	GTA	TCA	TTT	GAT	TCA	CTT	TTT	TCT															2163
Pro	Gln	Glu	Met	Lys	Thr	Tyr	Ser	Val	Ser	Phe	Asp	Ser	Leu	Phe	Ser															
			620			625					630																			
GCA	GTA	AAG	AAT	TTT	ACA	GAA	ATT	GCT	TCC	AAG	TTC	AGT	GAG	AGA	CTC															2211
Ala	Val	Lys	Asn	Phe	Thr	Glu	Ile	Ala	Ser	Lys	Phe	Ser	Glu	Arg	Leu															
					640					645					650															
CAG	GAC	TTT	GAC	AAA	AGC	AAC	CCA	ATA	GTA	TTA	AGA	ATG	ATG	AAT	GAT															2259
Gln	Asp	Phe	Asp	Lys	Ser	Asn	Pro	Ile	Val	Leu	Arg	Met	Met	Asn	Asp															
				655					660					665																

-106-

CAA CTC ATG TTT CTG GAA AGA GCA TTT ATT GAT CCA TTA GGG TTA CCA Gln Leu Met Phe Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro 670 675 680	2307
GAC AGG CCT TTT TAT AGG CAT GTC ATC TAT GCT CCA AGC AGC CAC AAC Asp Arg Pro Phe Tyr Arg His Val Ile Tyr Ala Pro Ser Ser His Asn 685 690 695	2355
AAG TAT GCA GGG GAG TCA TTC CCA GGA ATT TAT GAT GCT CTG TTT GAT Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp 700 705 710	2403
ATT GAA AGC AAA GTG GAC CCT TCC AAG GCC TGG GGA GAA GTG AAG AGA Ile Glu Ser Lys Val Asp Pro Ser Lys Ala Trp Gly Glu Val Lys Arg 715 720 725 730	2451
CAG ATT TAT GTT GCA GCC TTC ACA GTG CAG GCA GCT GCA GAG ACT TTG Gln Ile Tyr Val Ala Ala Phe Thr Val Gln Ala Ala Ala Glu Thr Leu 735 740 745	2499
AGT GAA GTA GCC TAAGAGGATT CTTTAGAGAA TCCGTATTGA ATTTGTGTGG Ser Glu Val Ala 750	2551
TATGTCACCTC AGAAAGAATC GTAATGGGTA TATTGATAAA TTTTAAAATT GGTATATTTG	2611
AAATAAAGTT GAATATTATA TATAAAAAAA AAAAAAAAAA AA	2653

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg 1 5 10 15
Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe 20 25 30
Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu 35 40 45
Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu 50 55 60
Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile 65 70 75 80
Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile 85 90 95
Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His 100 105 110
Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile

-107-

115					120					125					
Ser	Ile	Ile	Asn	Glu	Asp	Gly	Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe
130						135					140				
Glu	Pro	Pro	Pro	Pro	Gly	Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro
145					150					155				160	
Phe	Ser	Ala	Phe	Ser	Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr
				165					170					175	
Val	Asn	Tyr	Ala	Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met
			180					185					190		
Lys	Ile	Asn	Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val
		195					200					205			
Phe	Arg	Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly
	210					215					220				
Val	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys
225					230					235				240	
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	Gly
			245						250					255	
Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	Gly	Tyr
		260						265					270		
Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	Ala	Val	Gly
		275					280					285			
Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	Asp	Ala	Gln	Lys
	290					295					300				
Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	Asp	Ser	Ser	Trp	Arg
305					310					315				320	
Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	Pro	Gly	Phe	Thr	Gly	Asn
			325						330					335	
Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile	His	Ser	Thr	Asn	Glu	Val
			340					345					350		
Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro
	355						360					365			
Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly
	370					375					380				
Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg
385					390					395				400	
Ser	Phe	Gly	Thr	Leu	Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile
			405						410					415	
Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr
		420					425					430			
Glu	Trp	Ala	Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala
	435						440					445			

108

-108-

Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
 450 455 460
 Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
 465 470 475 480
 Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser
 485 490 495
 Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile
 500 505 510
 Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu
 515 520 525
 Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn
 530 535 540
 Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu
 545 550 555 560
 Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val
 565 570 575
 Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
 580 585 590
 Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
 595 600 605
 Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
 610 615 620
 Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
 625 630 635 640
 Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
 645 650 655
 Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
 660 665 670
 Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
 675 680 685
 His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
 690 695 700
 Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
 705 710 715 720
 Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
 725 730 735
 Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
 740 745 750

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid

109

-109-

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
Ser Leu Tyr Glu Ser Xaa Thr Lys
1 5
- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (F) TISSUE TYPE: Carcinoma
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
Ser Tyr Pro Asp Gly Xaa Asn Leu Pro Gly Gly Gly Val Gln Arg
1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO

-110-

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapien
 (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 (B) CLONE: Prostate Specific Membrane Antigen
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

 Phe Tyr Asp Pro Met Phe Lys
 1 5
- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapien
 (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 (B) CLONE: Prostate Specific Membrane Antigen
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

 Ile Tyr Asn Val Ile Gly Thr Leu Lys
 1 5
- (2) INFORMATION FOR SEQ ID NO:7:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapien
 (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 (B) CLONE: Prostate Specific Membrane Antigen
- 111

-111-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Phe Leu Tyr Xaa Xaa Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln
1 5 10 15
Asn Phe Gln Leu Ala Lys
 20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Asp Val
1 5 10 15
Lys

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

-112-

Pro Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val
 1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile
 1 5 10 15

Glu Ser Lys

113

- 113 -

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Xaa Xaa Glu
1 5 10 15
Ser Thr Glu Glu Ala Glu
20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTYTAYGAYC CNATGTT

17

(2) INFORMATION FOR SEQ ID NO:14:

- (i). SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

-114-

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapien
 (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AACATNGGRT CRTARAA

17

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapien
 (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATHTAYAAYG TNATHGG

17

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapien

115

-115-

(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCDATNACRT TRTADAT

17

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCNGCNGAYT AYTYYGC

17

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCRAARTART CNGCNGG

17

116

-116-

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACNGARCARA AYTTCARCT

20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGYTGRAART TYTGTCNGT

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

117

-117-

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GARCARAAAT TYCARCT

17

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGYTGRAAT TYTGYTC

17

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

118

-118-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGGGAYGCNG ARGARTTYGG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCRAAYTCYT CNGCRTCCCA

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGGGAYGCNG ARGARTT

17

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid

-119-

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapien
 - (F) TISSUE TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAYTCYTCNG CRTCCCA

17

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 780 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TACACTTATC CCATTTCGGAC ATGCCCCACCT TGGAACCTGGA GACCCTTACA CCCCAGGCTT	60
CCCTTCGTTT AACCACACCC ANNNGTTTCC ACCAGTTGAA TCTTCAGGAC TACCCACAT	120
TGCTGTTT CAG ACCATCTCTA GCAGTGCAGC AGCCAGGCTG TTCAGCAAAA TGGATGGAGA	180
CACATGCTCT GANAGNNGTT GGAAAGGTGC GATCCANNNT TCCTGTAAGG TNNGACNNAA	240
CAAAGCAGGA GANNNGCCA GANTAATGGT GAAACTAGAT GTGAACAATT CCATGAAAGA	300
CAGGAAGATT CTGAACATCT TCGGTGCTAT CCAGGGATT TGAAGAACCTG ATCGGTATGT	360
TGTGATTGGA GCCCAGAGAG ACTCCTGGGG CCCAGGAGTG GCTAAAGCTG GCACTGGAAC	420
TGCTATATTG TTGGAACCTG CCCGTGTGAT CTCAGACATA GTGAAAAACG AGGGCTACAA	480
ACCGAGGCGA AGCATCATCT TTGCTAGCTG GAGTGCAGGA GACTACGGAG CTGTGGGTGC	540
TACTGAATGG CTGGAGGGGT ACTCTGCCAT GCTGCATGCC AAAGCTTTCA CTTACATCAN	600
NGCTTGGATG CTCCAGTCCT GGGAGCAAGC CATGTCAAGA TTTCTGCCAG CCCCTTGCTG	660
TATATGCTGC TGGGGAGTAT TATGAAGGGG GTGAAGAATC CAGCAGCAGT CTCAGAGAGC	720

-120-

NNNNCTCTAT AACAGACTTG GCCCAGACTG GGTAAGCA GTTGTTCTC TTGGCCTGGA 780

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TGCAGAAAAG CTATTCAAAA ACATGGAAGG AAACGTGCCT CCTAGTTGGA ATATAGATTC	60
CTCATGTAAG CTGGAACCTT CACAGAATCA AAATGTGAAG CTCACGTGTA ACAATGTACT	120
GAAAGAAACA AGAATACTTA ACATCTTTGG CGTTATTAAA GGCTATGAGG AACCAGACCG	180
CTACATTGTA GTAGGAGCCC AGAGAGACGC TTGGGGCCCT GGTNGTTGCG AAGTCCAGTG	240
TGGGAACAGG TCTTCTGTT GAACTTGCC CAAGTATTCT CAGATATGAT TTCAAAGAT	300
GGATTTAGAC CCAGCAGGAG TATTATCTTT GCCAGCTGGA CTGCAGGAGA CTATGGAGCT	360
GTGGGTCCGA CTGAGTGGCT GGAGGGGTAC CTTTCATCTT TGCATCTAAA GNNNGCTTTC	420
ACTTACATTA ATNCTGGATA AAGTCGTCCT GGGTACTAGC AACTTCAAGG TTTCTGCCAG	480
CCCCCTATTA TATACACTTA TGGGGAAGAT AATGCAGGAN NCGTAAAGCA TCCGANNNNN	540
NNNTTGATGG AAAATATCTA TATCGAAACA GTAATTGGAT TAGCAAAATT GAGGAACTTT	600
CCTTGACAA TGCTGCATTC CCTTTTCTTG CATATTCAGG AATCCCAGCA GTTCTTTTCT	660

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

-121-

TATGGAAGGA GACTGTCCCT CTGACTGGAA AACAGACTCT ACATGTAGGA TGGTAACCTC	60
AGAAAGCAAG AATGTGAAGC TCACTGTGAG CAATGTGCTG AAAGAGATAA AAATTCTTAA	120
CATCTTTGGA GTTATTAAAG GCTTTGTAGA ACCAGATCAC TATGTTGTAG TTGGGGCCCA	180
GAGAGATGCA TGGGGCCCTG GAGCTGCAAA ATCNCGGTGT AGGCACAGCT CTCCTATTGA	240
AACTTGCCCA GATGTTCTCA GATATGGTCT TAAAAGATGG GTTTCAGCCC AGCAGAAGCA	300
TTATCTTTGC CAGTTGGAGT GCTGGAGACT TTGGATCGGT TGGTGCCACT GAATGGCTAG	360
AGGGATACCT TTCGTNCCT GCATTTAAAG GCTTTCACCT ATATTAATCT GGATAAAGCG	420
GTTCTTGTA CCAGCAACTT CAAGGTTTCT GCCAGCCAC TGTGTATAC GCTTATTGAG	480
AAAACAATGC AAAATGTGAA GCATCCGGTT ACTGGGCAAT TTCTATATCA GGACAGCAAC	540

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapien
- (F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ACGGAGCAAA ACTTTCAGCT TGCAAAG

27

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapien
- (F) TISSUE TYPE: Carcinoma

-122-

(vii) IMMEDIATE SOURCE:
(B) CLONE: Prostate Membrane Specific Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Thr Glu Gln Asn Phe Gln Leu Ala Lys
1 5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapien
(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:
(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCTTCGGCA TCCCAGCTTG CAAACAAAAT TGTTCT

36

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapien
(F) TISSUE TYPE: Carcinoma

(vii) IMMEDIATE SOURCE:
(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGAACAATTT TGTTTGCAAG CTGGGATGCC AAGGAG

36

(2) INFORMATION FOR SEQ ID NO:34:

-123-

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapien
 - (G) CELL TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg	Thr	Ile	Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu
1				5						10	
- (2) INFORMATION FOR SEQ ID NO:35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapien
 - (G) CELL TYPE: Carcinoma
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Asp	Glu	Leu	Lys	Ala	Glu
1				5	
- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

- 124 -

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapien
 - (G) CELL TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Asn Glu Asp Gly Asn Glu
1 5

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapien
 - (G) CELL TYPE: Carcinoma
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Lys Ser Pro Asp Glu Gly
1 5

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapien
 - (G) CELL TYPE: Carcinoma

125

-125-

(vii) IMMEDIATE SOURCE:

(B) CLONE: Prostate Specific Membrane Antigen

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ala Gly Ala Leu Val Leu Ala Gly Gly Phe Phe Leu Leu Gly Phe Leu
1 5 10 15

Phe